

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

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Application Serial Number: 10/567,749
Source: IFWP
Date Processed by STIC: 02/28/2006

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FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

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Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>**> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
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Revised 01/10/06



IFWP

RAW SEQUENCE LISTING

DATE: 02/28/2006

PATENT APPLICATION: US/10/567,749

TIME: 12:03:09

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Output Set: N:\CRF4\02282006\J567749.raw

3 <110> APPLICANT: Degussa AG <120> Process for the preparation of L-threonine <130>
030235

C--> 4 <140> CURRENT APPLICATION NUMBER: US/10/567,749

C--> 4 <141> CURRENT FILING DATE: 2006-02-10

E--> 4 <160> NUMBER OF SEQ ID: 10 <170> PatentIn version 3.1 <210> 1 <211> 993 <212> DNA <213>

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96 Phe Asp Glu Asn Gly Val Glu Val Phe Asp Glu Lys Ala Leu Val Glu
97 20 25 30
99 Gln Glu Pro Ser Asp Asn Asp Leu Ala Glu Glu Glu Leu Leu Ser Gln
100 35 40 45
102 Gly Ala Thr Gln Arg Val Leu Asp Ala Thr Gln Leu Tyr Leu Gly Glu
103 50 55 60
105 Ile Gly Tyr Ser Pro Leu Thr Ala Glu Glu Val Tyr Phe Ala
106 65 70 75 80
109 Arg Arg Ala Leu Arg Gly Asp Val Ala Ser Arg Arg Arg Met Ile Glu
110 85 90 95
112 Ser Asn Leu Arg Leu Val Val Lys Ile Ala Arg Arg Tyr Gly Asn Arg
113 100 105 110
115 Gly Leu Ala Leu Leu Asp Leu Ile Glu Glu Gly Asn Leu Gly Leu Ile
116 115 120 125
118 Arg Ala Val Glu Lys Phe Asp Pro Glu Arg Gly Phe Arg Phe Ser Thr
119 130 135 140
121 Tyr Ala Thr Trp Trp Ile Arg Gln Thr Ile Glu Arg Ala Ile Met Asn
122 145 150 155 160
124 Gln Thr Arg Thr Ile Arg Leu Pro Ile His Ile Val Lys Glu Leu Asn
125 165 170 175
127 Val Tyr Leu Arg Thr Ala Arg Glu Leu Ser His Lys Leu Asp His Glu
128 180 185 190
130 Pro Ser Ala Glu Glu Ile Ala Glu Gln Leu Asp Lys Pro Val Asp Asp
131 195 200 205
133 Val Ser Arg Met Leu Arg Leu Asn Glu Arg Ile Thr Ser Val Asp Thr
134 210 215 220

Does Not Comply
Corrected Diskette Needed

(p2-1-11)

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136 Pro Leu Gly Gly Asp Ser Glu Lys Ala Leu Leu Asp Ile Leu Ala Asp
 137 225 230 235 240
 139 Glu Lys Glu Asn Gly Pro Glu Asp Thr Thr Gln Asp Asp Asp Met Lys
 140 245 250 255
 142 Gln Ser Ile Val Lys Trp Leu Phe Glu Leu Asn Ala Lys Gln Arg Glu
 143 260 265 270
 145 Val Leu Ala Arg Arg Phe Gly Leu Leu Gly Tyr Glu Ala Ala Thr Leu
 146 275 280 285
 148 Glu Asp Val Gly Arg Glu Ile Gly Leu Thr Arg Glu Arg Val Arg Gln
 149 290 295 300
 151 Ile Gln Val Glu Gly Leu Arg Arg Leu Arg Glu Ile Leu Gln Thr Gln
 152 305 310 315 320
 154 Gly Leu Asn Ile Glu Ala Leu Phe Arg Glu
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E--> 162

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 165 ggagttgagg tttttgacga aaaggcctta gtagaatagg aaccagtgta taacgatttg 120
 167 gccgaagagg aactgttatc gcaggagacc acacagcgtg tgttgacgc gactcagctt 180
 169 taccttggtg agattggtta ttcaccactg ttaacggccg aagaagaagt ttattttgcg 240
 171 cgtcgcgcac tgcgtggaga tgcgcctct cgccgccgga tgatcgagag taacttgcgt 300
 173 ctggtggtaa aaattgcccg ccgttatggc aatcgtggtc tggcgttgct ggaccttatc 360
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 185 tcggtagaca ccccgctggg tgggtgattcc gaaaaagcgt tgctggacat cctggccgat 720
 187 gaaaaagaga acggtccgga agataccacg caagatgacg atatgaagca gagcatcgtc 780
 189 aaatggctgt tcgagctgaa cgccaaacag cgtgaagtgc tggcacgtcg attcggtttg 840
 191 ctgggggtacg aagcggcaac actggaagat gtaggtcgtg aaattggcct caccggtgaa 900
 193 cgtgttcgcc agattcaggt tgaaggcctg cgccgtttgc gcgaaatcct gcaaacgcag 960
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 208 <223> OTHER INFORMATION: ilvA-Gen

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RAW SEQUENCE LISTING

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215	tta aga gca gtg ctg cgc gcg ccg gtt tac gag gcg gcg cag gtt acg	96
216	Leu Arg Ala Val Leu Arg Ala Pro Val Tyr Glu Ala Ala Gln Val Thr	
217	20 25 30	
219	ccg cta caa aaa atg gaa aaa ctg tgc tgc cgt ctt gat aac gtc att	144
220	Pro Leu Gln Lys Met Glu Lys Leu Ser Ser Arg Leu Asp Asn Val Ile	
221	35 40 45	
223	ctg gtg aag cgc gaa gat cgc cag cca gtg cac agc ttt aag ctg cgc	192
224	Leu Val Lys Arg Glu Asp Arg Gln Pro Val His Ser Phe Lys Leu Arg	
225	50 55 60	
227	ggc gca tac gcc atg atg gcg ggc ctg acg gaa gaa cag aaa gcg cac	240
228	Gly Ala Tyr Ala Met Met Ala Gly Leu Thr Glu Glu Gln Lys Ala His	
229	65 70 75 80	
231	ggt gta atc act ggt tct gcg ggt aac cac gcg cag ggc gac gcg ttt	288
232	Gly Val Ile Thr Ala Ser Ala Gly Asn His Ala Gln Gly Val Ala Phe	
233	85 90 95	
235	tct tct gcg cgg tta ggc gtg aag gcc ctg atc gtt atg cca acc gcc	336
236	Ser Ser Ala Arg Leu Gly Val Lys Ala Leu Ile Val Met Pro Thr Ala	
237	100 105 110	
239	acc gcc gac atc aaa gtc gac gcg gtg cgc ggc ttc ggc ggc gaa gtg	384
240	Thr Ala Asp Ile Lys Val Asp Ala Val Arg Gly Phe Gly Gly Glu Val	
241	115 120 125	
243	ctg ctc cac ggc gcg aac ttt gat gaa gcg aaa gcc aaa gcg atc gaa	432
244	Leu Leu His Gly Ala Asn Phe Asp Glu Ala Lys Ala Lys Ala Ile Glu	
245	130 135 140	
247	ctg tca cag cag cag ggg ttc acc tgg gtg ccg ccg ttc gac cat ccg	480
248	Leu Ser Gln Gln Gln Gly Phe Thr Trp Val Pro Pro Phe Asp His Pro	
249	145 150 155 160	
251	atg gtg att gcc ggg caa ggc acg ctg gcg gaa ctg ctc cag cag	528
252	Met Val Ile Ala Gly Gln Gly Thr Leu Ala Leu Glu Leu Leu Gln Gln	
253	165 170 175	
255	gac gcc cat ctc gac cgc gta ttt gtg cca gtc ggc ggc ggc ggt ctg	576
256	Asp Ala His Leu Asp Arg Val Phe Val Pro Val Gly Gly Gly Gly Leu	
257	180 185 190	
259	gct gct ggc gtg gcg gtg ctg atc aaa caa ctg atg ccg caa atc aaa	624
260	Ala Ala Gly Val Ala Val Leu Ile Lys Gln Leu Met Pro Gln Ile Lys	
261	195 200 205	
264	gtg atc gcc gta gaa gcg gaa gac tcc gcc tgc ctg aaa gca gcg ctg	672
265	Val Ile Ala Val Glu Ala Glu Asp Ser Ala Cys Leu Lys Ala Ala Leu	
266	210 215 220	
268	gat gcg ggt cat ccg gtt gat ctg ccg cgc gta ggg cta ttt gct gaa	720
269	Asp Ala Gly His Pro Val Asp Leu Pro Arg Val Gly Leu Phe Ala Glu	
270	225 230 235 240	
272	ggc gta gcg gta aaa cgc atc ggt gac gaa acc ttc cgt tta tgc cag	768

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277 Glu Tyr Leu Asp Asp Ile Ile Thr Val Asp Ser Asp Ala Ile Cys Ala
278          260          265          270
280 gcg atg aag gat tta ttc gaa gat gtg cgc gcg gtg gcg gaa ccc tct      864
281 Ala Met Lys Asp Leu Phe Glu Asp Val Arg Ala Val Ala Glu Pro Ser
282          275          280          285
284 ggc gcg ctg gcg ctg gcg gga atg aaa aaa tat atc gcc ctg cac aac      912
285 Gly Ala Leu Ala Leu Ala Gly Met Lys Lys Tyr Ile Ala Leu His Asn
286          290          295          300
288 att cgc ggc gaa cgg ctg gcg cat att ctt tcc ggt gcc aac gtg aac      960
289 Ile Arg Gly Glu Arg Leu Ala His Ile Leu Ser Gly Ala Asn Val Asn
290 305          310          315          320
292 ttc cac ggc ctg cgc tac gtc tca gaa cgc tgc gaa ctg ggc gaa cag      1008
293 Phe His Gly Leu Arg Tyr Val Ser Glu Arg Cys Glu Leu Gly Glu Gln
294          325          330          335
296 cgt gaa gcg ttg ttg gcg gtg acc att ccg gaa gaa aaa ggc agc ttc      1056
297 Arg Glu Ala Leu Leu Ala Val Thr Ile Pro Glu Glu Lys Gly Ser Phe
298          340          345          350
300 ctc aaa ttc tgc caa ctg ctt ggc ggg cgt tgc gtc acc gag ttc aac      1104
301 Leu Lys Phe Cys Gln Leu Leu Gly Gly Arg Ser Val Thr Glu Phe Asn
302          355          360          365
304 tac cgt ttt gcc gat gcc aaa aac gcc tgc atc ttt gtc ggt gtg cgc      1152
305 Tyr Arg Phe Ala Asp Ala Lys Asn Ala Cys Ile Phe Val Gly Val Arg
306          370          375          380
308 ctg agc cgc ggc ctc gaa gag cgc aaa gaa att ttg cag atg ctc aac      1200
309 Leu Ser Arg Gly Leu Glu Glu Arg Lys Glu Ile Leu Gln Met Leu Asn
310 385          390          395          400
312 gac ggc ggc tac agc gtg gtt gat ctc tcc gac gac gaa atg gcg aag      1248
313 Asp Gly Gly Tyr Ser Val Val Asp Leu Ser Asp Asp Glu Met Ala Lys
314          405          410          415
316 cta cac gtg cgc tat atg gtc ggc gga cgt cca tgc cat ccg ttg cag      1296
317 Leu His Val Arg Tyr Met Val Gly Gly Arg Pro Ser His Pro Leu Gln
318          420          425          430
320 gaa cgc ctc tac agc ttc gaa ttc ccg gaa tca ccg ggc gcg ctg ctg      1344
321 Glu Arg Leu Tyr Ser Phe Glu Phe Pro Glu Ser Pro Gly Ala Leu Leu
322          435          440          445
324 cgc ttc ctc aac acg ctg ggt acg tac tgg aac att tct ttg ttc cac      1392
325 Arg Phe Leu Asn Thr Leu Gly Thr Tyr Trp Asn Ile Ser Leu Phe His
326          450          455          460
329 tat cgc agc cat ggc acc gac tac ggg cgc gta ctg gcg gcg ttc gaa      1440
330 Tyr Arg Ser His Gly Thr Asp Tyr Gly Arg Val Leu Ala Ala Phe Glu
331 465          470          475          480
333 ctt ggc gac cat gaa ccg gat ttc gaa acc ccg ctg aat gag ctg ggc      1488
334 Leu Gly Asp His Glu Pro Asp Phe Glu Thr Arg Leu Asn Glu Leu Gly
335          485          490          495
337 tac gat tgc cac gac gaa acc aat aac ccg gcg ttc agg ttc ttt ttg      1536
338 Tyr Asp Cys His Asp Glu Thr Asn Asn Pro Ala Phe Arg Phe Phe Leu

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341 gcg ggt tag

342 Ala Gly

E--> 345 <210> SEQ ID NO: 6<211> 514<212> PRT<213> Escherichia coli

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E--> 346 .

W--> 346 <400> SEQUENCE: 6

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353 Pro Leu Gln Lys Met Glu Lys Leu Ser Ser Arg Leu Asp Asn Val Ile

354 35 40 45

356 Leu Val Lys Arg Glu Asp Arg Gln Pro Val His Ser Phe Lys Leu Arg

357 50 55 60

359 Gly Ala Tyr Ala Met Met Ala Gly Leu Thr Glu Glu Lys Ala His

360 65 70 75 80

362 Gly Val Ile Thr Ala Ser Ala Gly Asn His Ala Glu Gly Val Ala Phe

363 85 90 95

365 Ser Ser Ala Arg Leu Gly Val Lys Ala Leu Ile Val Met Pro Thr Ala

366 100 105 110

368 Thr Ala Asp Ile Lys Val Asp Ala Val Arg Gly Phe Gly Gly Glu Val

369 115 120 125

371 Leu Leu His Gly Ala Asn Phe Asp Glu Ala Lys Ala Lys Ala Ile Glu

372 130 135 140

374 Leu Ser Gln Gln Gln Gly Phe Thr Trp Val Pro Pro Phe Asp His Pro

375 145 150 155 160

377 Met Val Ile Ala Gly Gln Gly Thr Leu Ala Leu Glu Leu Leu Gln Gln

378 165 170 175

380 Asp Ala His Leu Asp Arg Val Phe Val Pro Val Gly Gly Gly Glu Leu

381 180 185 190

383 Ala Ala Gly Val Ala Val Leu Ile Lys Gln Leu Met Pro Gln Ile Lys

384 195 200 205

386 Val Ile Ala Val Glu Ala Glu Asp Ser Ala Cys Leu Lys Ala Ala Leu

387 210 215 220

390 Asp Ala Gly His Pro Val Asp Leu Pro Arg Val Gly Leu Phe Ala Glu

391 225 230 235 240

393 Gly Val Ala Val Lys Arg Ile Gly Asp Glu Thr Phe Arg Leu Cys Gln

394 245 250 255

396 Glu Tyr Leu Asp Asp Ile Ile Thr Val Asp Ser Asp Ala Ile Cys Ala

397 260 265 270

399 Ala Met Lys Asp Leu Phe Glu Asp Val Arg Ala Val Ala Glu Pro Ser

400 275 280 285

402 Gly Ala Leu Ala Leu Ala Gly Met Lys Lys Tyr Ile Ala Leu His Asn

403 290 295 300

405 Ile Arg Gly Glu Arg Leu Ala His Ile Leu Ser Gly Ala Asn Val Asn

406 305 310 315 320

408 Phe His Gly Leu Arg Tyr Val Ser Glu Arg Cys Glu Leu Gly Glu Gln

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412          340          345          350
414 Leu Lys Phe Cys Gln Leu Leu Gly Gly Arg Ser Val Thr Glu Phe Asn
415          355          360          365
417 Tyr Arg Phe Ala Asp Ala Lys Asn Ala Cys Ile Phe Val Gly Val Arg
418          370          375          380
420 Leu Ser Arg Gly Leu Glu Glu Arg Lys Glu Ile Leu Gln Met Leu Asn
421 385          390          395          400
423 Asp Gly Gly Tyr Ser Val Val Asp Leu Ser Asp Asp Glu Met Ala Lys
424          405          410          415
426 Leu His Val Arg Tyr Met Val Gly Gly Arg Pro Ser His Pro Leu Gln
427          420          425          430
429 Glu Arg Leu Tyr Ser Phe Glu Phe Pro Glu Ser Pro Gly Ala Leu Leu
430          435          440          445
432 Arg Phe Leu Asn Thr Leu Gly Thr Tyr Trp Asn Ile Ser Leu Phe His
433          450          455          460
435 Tyr Arg Ser His Gly Thr Asp Tyr Gly Arg Val Leu Ala Ala Phe Glu
436 465          470          475          480
438 Leu Gly Asp His Glu Phe Asp Phe Glu Thr Arg Leu Asn Glu Leu Gly
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462          20          25          30
464 ccg cta caa aaa atg gaa aaa ctg tcg tcg cgt ctt gat aac gtc att 144
465 Pro Leu Gln Lys Met Glu Lys Leu Ser Ser Arg Leu Asp Asn Val Ile
466          35          40          45
468 ctg gtg aag cgc gaa gat cgc cag cca gtg cac agc ttt aag ctg cgc 192
469 Leu Val Lys Arg Glu Asp Arg Gln Pro Val His Ser Phe Lys Leu Arg
470          50          55          60
472 ggc gca tac gcc atg atg gcg ggc ctg acg gaa gaa cag aaa gcg cac 240
473 Gly Ala Tyr Ala Met Met Ala Gly Leu Thr Glu Glu Gln Lys Ala His
474 65          70          75          80
476 ggc gtg atc act gct tct gcg ggt aac cac gcg cag ggc gtc gcg ttt 288
477 Gly Val Ile Thr Ala Ser Ala Gly Asn His Ala Gln Gly Val Ala Phe
478          85          90          95

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Same
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485 Thr Ala Asp Ile Lys Val Asp Ala Val Arg Gly Phe Gly Gly Glu Val
486          115          120          125
488 ctg ctc cac ggc gcg aac ttt gat gaa gcg aaa gcc aaa gcg atc gaa      432
489 Leu Leu His Gly Ala Asn Phe Asp Glu Ala Lys Ala Lys Ala Ile Glu
490          130          135          140
492 ctg tca cag cag cag ggg ttc acc tgg gtg ccg ccg ttc gac cat ccg      480
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501 Asp Ala His Leu Asp Arg Val Phe Val Pro Val Gly Gly Gly Gly Leu
502          180          185          190
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506          195          200          205
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510 Val Ile Ala Val Glu Ala Glu Asp Ser Ala Cys Leu Lys Ala Ala Leu
511          210          215          220
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514 Asp Ala Gly His Pro Val Asp Leu Pro Arg Val Gly Leu Phe Ala Glu
515 225          230          235          240
517 ggc gta gcg gta aaa cgc atc ggt gac gaa acc ttc cgt tta tgc cag      768
518 Gly Val Ala Val Lys Arg Ile Gly Asp Glu Thr Phe Arg Leu Cys Gln
519          245          250          255
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522 Glu Tyr Leu Asp Asp Ile Ile Thr Val Asp Ser Asp Ala Ile Cys Ala
523          260          265          270
525 gcg atg aag gat tta ttc gaa gat gtg cgc gcg gtg gcg aaa ccc tct      864
526 Ala Met Lys Asp Leu Phe Glu Asp Val Arg Ala Val Ala Lys Pro Ser
527          275          280          285
529 ggc gcg ctg gcg ctg gcg gga atg aaa aaa tat atc gcc ctg cac aac      912
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531          290          295          300
533 att cgc ggc gaa cgg ctg gcg cat att ctt tcc ggt gcc aac gtg aac      960
534 Ile Arg Gly Glu Arg Leu Ala His Ile Leu Ser Gly Ala Asn Val Asn
535 305          310          315          320
537 ttc cac ggc ctg cgc tac gtc tca gaa cgc tgc gaa ctg ggc gaa cag      1008
538 Phe His Gly Leu Arg Tyr Val Ser Glu Arg Cys Glu Leu Gly Glu Gln
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555 385          390          395          400
557 gac ggc ggc tac agc gtg gtt gat ctc tcc gac gac gaa atg gcg aag      1248
558 Asp Gly Gly Tyr Ser Val Val Asp Leu Ser Asp Asp Glu Met Ala Lys
559          405          410          415
561 cta cac gtg cgc tat atg gtc ggc gga cgt cca tcg cat ccg ttg cag      1296
562 Leu His Val Arg Tyr Met Val Gly Gly Arg Pro Ser His Pro Leu Gln
563          420          425          430
565 gaa cgc ctc tac agc ttc gaa ttc ccg gaa tca ccg ggc gcg ctg ctg      1344
566 Glu Arg Leu Tyr Ser Phe Glu Phe Pro Glu Ser Pro Gly Ala Leu Leu
567      435          440          445
569 cgc ttc ctc aac acg ctg ggt acg tac tgg aac att tct ttg ttc cac      1392
570 Arg Phe Tyr Asn Thr Leu Gly Thr Tyr Trp Asn Ile Ser Leu Phe Thr
571      450          455          460
574 tat cgc agc cat ggc acc gac tac ggg cgc gta ctg gcg gcg ttc gaa      1440
575 Tyr Arg Ser His Gly Thr Asp Tyr Gly Arg Val Leu Ala Ala Phe Glu
576 465          470          475          480
578 ctt ggc gac cat gaa ccg gat ttc gaa acc ccg ctg aat gag ctg ggc      1488
579 Leu Gly Asp His Glu Pro Asp Phe Glu Thr Arg Leu Asn Glu Leu Gly
580          485          490          495
582 tac gat tgc cac gac gaa acc aat aac ccg gcg ttc agg ttc ttt ttg      1536
583 Tyr Asp Cys His Asp Glu Thr Asn Asn Pro Ala Phe Arg Phe Phe Leu
584          500          505          510
586 gcg ggt tag
587 Ala Gly

```

hard Return Euler

E--> 590 <210> SEQ ID NO: 8<211> 514<212> PRT<213> Escherichia coli

E--> 591

E--> 591

E--> 591

W--> 591 <400> SEQUENCE: 8

```

592 Met Ala Asp Ser Gln Pro Leu Ser Gly Ala Pro Glu Gly Ala Glu Tyr
593 1          5          10          15
595 Leu Arg Ala Val Leu Arg Ala Pro Val Tyr Glu Ala Ala Gln Val Thr
596      20          25          30
598 Pro Leu Gln Lys Met Glu Lys Leu Ser Ser Arg Leu Asp Asn Val Ile
599      35          40          45
601 Leu Val Lys Arg Glu Asp Arg Gln Pro Val His Ser Phe Lys Leu Arg
602      50          55          60
604 Gly Ala Tyr Ala Met Met Ala Gly Leu Thr Glu Glu Gln Lys Ala His
605 65          70          75          80
607 Gly Val Ile Thr Ala Ser Ala Gly Asn His Ala Gln Gly Val Ala Phe
608          85          90          95
610 Ser Ser Ala Arg Leu Gly Val Lys Ala Leu Ile Val Met Pro Thr Ala

```

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/567,749

DATE: 02/28/2006

TIME: 12:03:09

Input Set : A:\pto.da.txt

Output Set: N:\CRF4\02282006\J567749.raw

```

611          100          105          110
613 Thr Ala Asp Ile Lys Val Asp Ala Val Arg Gly Phe Gly Gly Glu Val
614          115          120          125
616 Leu Leu His Gly Ala Asn Phe Asp Glu Ala Lys Ala Lys Ala Ile Glu
617          130          135          140
619 Leu Ser Gln Gln Gln Gly Phe Thr Trp Val Pro Pro Phe Asp His Pro
620 145          150          155          160
622 Met Val Ile Ala Gly Gln Gly Thr Leu Ala Leu Glu Leu Leu Gln Gln
623          165          170          175
625 Asp Ala His Leu Asp Arg Val Phe Val Pro Val Gly Gly Gly Gly Leu
626          180          185          190
629 Ala Ala Gly Val Ala Val Leu Ile Lys Gln Leu Met Pro Gln Ile Lys
630          195          200          205
632 Val Ile Ala Val Glu Ala Glu Asp Ser Ala Cys Leu Lys Ala Ala Leu
633          210          215          220
635 Asp Ala Gly His Pro Val Asp Leu Pro Arg Val Gly Leu Phe Ala Glu
636 225          230          235          240
638 Gly Val Ala Val Lys Arg Ile Gly Asp Glu Thr Phe Arg Leu Cys Gln
639          245          250          255
641 Glu Tyr Leu Asp Asp Ile Ile Thr Val Asp Ser Asp Ala Ile Cys Ala
642          260          265          270
644 Ala Met Lys Asp Leu Phe Glu Asp Val Arg Ala Val Ala Lys Pro Ser
645          275          280          285
647 Gly Ala Leu Ala Leu Ala Gly Met Lys Lys Tyr Ile Ala Leu His Asn
648          290          295          300
650 Ile Arg Gly Glu Arg Leu Ala His Ile Leu Ser Gly Ala Asn Val Asn
651 305          310          315          320
653 Phe His Gly Leu Arg Tyr Val Ser Glu Arg Cys Glu Leu Gly Glu Gln
654          325          330          335
656 Arg Glu Ala Leu Leu Ala Val Thr Ile Pro Glu Glu Lys Gly Ser Phe
657          340          345          350
659 Leu Lys Phe Cys Gln Leu Leu Gly Arg Ser Val Thr Glu Phe Asn
660          355          360          365
662 Tyr Arg Phe Ala Asp Ala Lys Asn Ala Cys Ile Phe Val Gly Val Arg
663          370          375          380
665 Leu Ser Arg Gly Leu Glu Glu Arg Lys Glu Ile Leu Gln Met Leu Asn
666 385          390          395          400
668 Asp Gly Gly Tyr Ser Val Val Asp Leu Ser Asp Asp Glu Met Ala Lys
669          405          410          415
671 Leu His Val Arg Tyr Met Val Gly Gly Arg Pro Ser His Pro Leu Gln
672          420          425          430
674 Glu Arg Leu Tyr Ser Phe Glu Phe Pro Glu Ser Pro Gly Ala Leu Leu
675          435          440          445
677 Arg Phe Leu Asn Thr Leu Gly Thr Tyr Trp Asn Ile Ser Leu Phe His
678          450          455          460
680 Tyr Arg Ser His Gly Thr Asp Tyr Gly Arg Val Leu Ala Ala Phe Glu
681 465          470          475          480
683 Leu Gly Asp His Glu Pro Asp Phe Glu Thr Arg Leu Asn Glu Leu Gly
684          485          490          495

```

RAW SEQUENCE LISTING

DATE: 02/28/2006

PATENT APPLICATION: US/10/567,749

TIME: 12:03:09

Input Set : A:\pto.da.txt

Output Set: N:\CRF4\02282006\J567749.raw

```

686 Tyr Asp Cys His Asp Glu Thr Asn Asn Pro Ala Phe Arg Phe Phe Leu
687          500                      505                      510
689 Ala Gly
E--> 692 <210> SEQ ID NO: 9<211> 1548<212> DNA<213> Escherichia coli
W--> 694 <220> FEATURE: <221> DNA<222> (1)..(1548)<223>
W--> 695
E--> 696
E--> 698
E--> 698
698 <400> SEQUENCE: 9
699 tcgcgatctg gtactgtaag gggaaataga gatgacacac gataataaat tgcagggttga      60
701 agctattaaa cgcggcacgg taattgacca tatccccgcc cagatcgggtt ttaagctggt      120
703 gagtctgttc aaagctgaccg aaacgggatca gcgcataccc attggtctga acctgccttc      180
705 tggcgagatg ggccgcaaaag atctgatcaa aatcgaaaat acctttttga gtgaagatca      240
707 agtagatcaa ctggcattgt atgcgccgca agccacgggtt aaccgtatcg acaactatga      300
709 agtgggtgggt aaatcgcgcc caagtctgcc ggagcgcata gacaatgtgc tgggtctgccc      360
711 gaacagcaac tgtatcagcc atgccgaacc ggtttcatcc agctttgccg tgcgaaaacg      420
713 cgccaatgat atcgcgctca aatgcaaata ctgtgaaaaa gagttttccc ataattgtggt      480
715 gctgggaaat taattggcgt tggtaataaa agtctggctc cctata atg agc agc      535
716                                     Met Ser Gln
717                                     1
719 act ttt tac cgc tgt aat aaa gga gaa atc atg agc aaa act atc gcg      583
720 Thr Phe Tyr Arg Cys Asn Lys Gly Glu Ile Met Ser Lys Thr Ile Ala
721      5                      10                      15
723 acg gaa aat gca ccg gca gct atc ggt cct tac gta cag ggc gtt gat      631
724 Thr Glu Asn Ala Pro Ala Ala Ile Gly Pro Tyr Val Gln Gly Val Asp
725 20                      25                      30                      35
727 ctg ggc aat atg atc atc acc tcc ggt cag atc ccg gta aat ccg aaa      679
728 Leu Gly Asn Met Ile Ile Thr Ser Gly Gln Ile Pro Val Asn Pro Lys
729      40                      45                      50
731 acg ggc gaa gta ccg gca gac gtc gct gca cag gca cgt cag tcg ctg      727
732 Thr Gly Glu Val Pro Ala Asp Val Ala Ala Gln Ala Arg Gln Ser Leu
733      55                      60                      65
735 gat aac gta aaa gcg atc gtc gaa gcc gct ggc ctg aaa gtg ggc gac      775
736 Asp Asn Val Lys Ala Ile Val Glu Ala Ala Gly Leu Lys Val Gly Asp
737      70                      75                      80
739 atc gtt aaa act acc gtg ttt gta aaa gat ctg aac gac ttc gca acc      823
740 Ile Val Lys Thr Thr Val Phe Val Lys Asp Leu Asn Asp Phe Ala Thr
741      85                      90                      95
743 gta aac gcc act tac gaa gcc ttc ttc acc gaa cac aac gcc acc ttc      871
744 Val Asn Ala Thr Tyr Glu Ala Phe Phe Thr Glu His Asn Ala Thr Phe
745 100                      105                      110                      115
747 ccg gca cgt tct tgc gtt gaa gtt gcc cgt ctg ccg aaa gac gtg aag      919
748 Pro Ala Arg Ser Cys Val Glu Val Ala Arg Leu Pro Lys Asp Val Lys
749      120                      125                      130
752 att gag atc gaa gcg atc gct gtt cgt cgc taa tcttgatgga aatccgggct      972
753 Ile Glu Ile Glu Ala Ile Ala Val Arg Arg
754      135                      140
756 atcatgcccg gattaagtct gatgacaaac gcaaaatcgc ctgatgcgct acgcttatca      1032

```

RAW SEQUENCE LISTING

DATE: 02/28/2006

PATENT APPLICATION: US/10/567,749

TIME: 12:03:09

Input Set : A:\pto.da.txt

Output Set: N:\CRF4\02282006\J567749.raw

```

758 ggcctacgtg attcctgcaa tttattgaat ttgttggccg gataaggcat ttacgccgca 1092
760 tccggcatga acaaaactca ctttgtctac aatctgaatc ggggctatcg tgcccagttt 1152
762 attctttatt gccagccgta acgacggcta tagaaccctt tcaccaactg ggттаатgtc 1212
764 atataccctg ccagaatcgc aaccagccac gggaaatagc ttaacggcag cgctgtaat 1272
766 tgcagataac tggccagcgg tgaaaacggc aatgcgatcc cgacaatcat cagcatcacg 1332
768 gtcatgatca ttaacggcca cgatgcacag ctctgaataa acggcacacg gcgggtgcgg 1392
770 atcatatgca caatcagcgt ttgcgacagt aagcccacca caaacatcc cgactggaac 1452
772 agcgtttgcg tttccggcgt gttggcatgg aataccacc acatcaggca aaacgtcaaa 1512
774 atatcgaaga tcgagctgat cgggtccgaag aagatc 1548
E--> 777 <210> SEQ ID NO: 10<211> 141<212> PRT<213> Escherichia coli
E--> 778
E--> 778
E--> 778
W--> 778 <400> SEQUENCE: 10
779 Met Ser Gln Thr Phe Tyr Arg Cys Asn Lys Gly Glu Ile Met Ser Lys
780 1 5 10 15
782 Thr Ile Ala Thr Glu Asn Ala Pro Ala Ala Ile Gly Pro Tyr Val Gln
783 20 25 30
785 Gly Val Asp Leu Gly Asn Met Ile Ile Thr Ser Gly Glu Ile Pro Val
786 35 40 45
788 Asn Pro Lys Thr Gly Glu Val Pro Ala Asp Val Ala Ala Gln Ala Arg
789 50 55 60
791 Gln Ser Leu Asp Asn Val Lys Ala Ile Val Glu Ala Ala Gly Leu Lys
792 65 70 75 80
794 Val Gly Asp Ile Val Lys Thr Thr Val Phe Val Lys Asp Leu Asn Asp
795 85 90 95
797 Phe Ala Thr Val Asn Ala Thr Tyr Glu Ala Phe Phe Thr Glu His Asn
798 100 105 110
800 Ala Thr Phe Pro Ala Arg Ser Cys Val Glu Val Ala Arg Leu Pro Lys
801 115 120 125
803 Asp Val Lys Ile Glu Ile Glu Ala Ile Ala Val Arg Arg
804 130 135 140

```

VERIFICATION SUMMARY

DATE: 02/28/2006

PATENT APPLICATION: US/10/567,749

TIME: 12:03:11

Input Set : A:\pto.da.txt

Output Set: N:\CRF4\02282006\J567749.raw

L:4 M:270 C: Current Application Number differs, Replaced Current Application No
 L:4 M:271 C: Current Filing Date differs, Replaced Current Filing Date
 L:0 M:282 E: Numeric Field Identifier Missing, <120> TITLE INVENTION
 L:0 M:201 W: Mandatory field data missing, <130> FILE REFERENCE
 L:4 M:283 W: Missing Blank Line separator, <160> field identifier
 L:5 M:281 W: Numeric Fields not Ordered, <220> not ordered!
 L:5 M:283 W: Missing Blank Line separator, <220> field identifier
 L:5 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
 L:7 M:282 E: Numeric Field Identifier Missing, <210> is required.
 L:7 M:282 E: Numeric Field Identifier Missing, <211> is required.
 L:7 M:282 E: Numeric Field Identifier Missing, <212> is required.
 L:7 M:282 E: Numeric Field Identifier Missing, <213> is required.
 L:7 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:1
 L:92 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO: 2<211> 330<212>
 PRT<213> Escherichia coli<400> 2
 L:93 M:282 E: Numeric Field Identifier Missing, <211> is required.
 L:93 M:282 E: Numeric Field Identifier Missing, <212> is required.
 L:93 M:282 E: Numeric Field Identifier Missing, <213> is required.
 L:93 M:200 E: Mandatory Header Field missing, <220> is required
 L:157 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO: 3<211> 993<212>
 DNA<213> Escherichia coli<220><221> Allele<222>
 L:160 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
 L:162 M:282 E: Numeric Field Identifier Missing, <211> is required.
 L:162 M:282 E: Numeric Field Identifier Missing, <212> is required.
 L:162 M:282 E: Numeric Field Identifier Missing, <213> is required.
 L:197 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO: 4<211> 75<212>
 DNA<213> Escherichia coli<220><221> tRNA<222>
 L:200 M:282 E: Numeric Field Identifier Missing, <211> is required.
 L:200 M:282 E: Numeric Field Identifier Missing, <212> is required.
 L:200 M:282 E: Numeric Field Identifier Missing, <213> is required.
 L:200 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:4
 L:207 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO: 5<211> 1545<212>
 DNA<213> Escherichia coli<220><221> CDS<222>
 L:210 M:282 E: Numeric Field Identifier Missing, <211> is required.
 L:210 M:282 E: Numeric Field Identifier Missing, <212> is required.
 L:210 M:282 E: Numeric Field Identifier Missing, <213> is required.
 L:210 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:5
 L:345 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO: 6<211> 514<212>
 PRT<213> Escherichia coli
 L:346 M:282 E: Numeric Field Identifier Missing, <211> is required.
 L:346 M:282 E: Numeric Field Identifier Missing, <212> is required.
 L:346 M:282 E: Numeric Field Identifier Missing, <213> is required.
 L:346 M:283 W: Missing Blank Line separator, <400> field identifier
 L:447 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO: 7<211> 1545<212>
 DNA<213> Escherichia coli
 L:449 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
 L:452 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
 L:455 M:282 E: Numeric Field Identifier Missing, <211> is required.
 L:455 M:282 E: Numeric Field Identifier Missing, <212> is required.
 L:455 M:282 E: Numeric Field Identifier Missing, <213> is required.
 L:590 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO: 8<211> 514<212>
 PRT<213> Escherichia coli
 L:591 M:282 E: Numeric Field Identifier Missing, <211> is required.

L:591 M:282 E: Numeric Field Identifier Missing, <212> is required.

L:591 M:282 E: Numeric Field Identifier Missing, <213> is required.

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/567,749

DATE: 02/28/2006

TIME: 12:03:11

Input Set : A:\pto.da.txt

Output Set: N:\CRF4\02282006\J567749.raw

L:591 M:283 W: Missing Blank Line separator, <400> field identifier
L:692 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO: 9<211> 1548<212>
DNA<213> Escherichia coli
L:694 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:695 M:283 W: Missing Blank Line separator, <220> field identifier
L:695 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:698 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:698 M:282 E: Numeric Field Identifier Missing, <212> is required.
L:698 M:282 E: Numeric Field Identifier Missing, <213> is required.
L:777 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO: 10<211> 141<212>
PRT<213> Escherichia coli
L:778 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:778 M:282 E: Numeric Field Identifier Missing, <212> is required.
L:778 M:282 E: Numeric Field Identifier Missing, <213> is required.
L:778 M:283 W: Missing Blank Line separator, <400> field identifier
L:4 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (10) Counted (9) ✓